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Genetic Diversity of Puumala Virus Isolates in the Republic of Tatarstan and the Republic of Mordovia

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Abstract

© 2016, Springer Science+Business Media New York.Puumala virus (PUUV) is the main causative agent of nephropathia epidemica (NE), a mild form of the hemorrhagic fever with renal syndrome (HFRS). The bank vole (Myodes glareolus) is the natural reservoir of PUUV. Several distinct lineages of PUUV have been identified that circulate in bank voles worldwide; however, little is known about genetic diversity of the PUUV strains that cause NE in the Volga Region of Russia. Partial PUUV S segment sequences (171 bp) were isolated from 25 NE serum samples collected in the Republic of Tatarstan (RT) and eight samples from the Republic of Mordovia (MR). Phylogenetic analysis revealed that 14 PUUV sequences from RT were clustered together with the strains previously identified circulating in Russia, including those from Samara Oblast, RT (Kazan) and the Republic of Udmurtia. Interestingly, 11 PUUV sequences were grouped together with the virus strain from Pieksamaki, which belongs to the PUUV genetic lineage circulating in Finland. The majority of PUUV sequences isolated from MR were clustered with the strains from RT (Kazan) and Udmurtia; however, few strains were genetically closer to the strains “Ufa97.11” or the Pieksamaki. Thus, PUUV associated with NE in RT and MR displays high genetic diversity, suggesting co-circulation of at least two distinct genetic lineages in the Volga Region of Russia.

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Keywords

Bunyaviridae, Hantaviruses, Hemorrhagic fever with renal syndrome (HFRS), Nephropathia Epidemica (NE), Puumala virus

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